FIGURE 1

1 TCTAGAGTCA AATGTGCCTT ATTATCAGTA CAAAAATAAA TGGTGTCAGC

51 TGGGTGCAGT GACTCACACC TGTAATCCCA GCACTTTAAG AGGCTGAGGC

101 AGGTGGATCA CCTGAGGCCA GGAGTTTGAG ACCAGCCTGG CCAACATGGT

151 GAAACCACAT TGTCAGGCCT CTGAGCCCAA GCCAAGCCAT CGCATCCCCT

201 GTGACTTGCA CGTATACATC CAGATGGCCT GAAGTAACTG AAGATCCACA

251 AAAGAAGTAA AAATAGCCTT AACTGATGAC ATTCCACCAT TGTGATTTGT

301 TTCTGCCCCA CCCGAACTGA TCAATGTACT TTGTAATCTC CCCCACCCTT

351 AAGAAGGTTC TTTGTAATTC TCCCCACCCT TGAGAATGTA CTTTGTGAGA

401 TCCACCCCTG CCCACAAAAC ATTGCTCTCA ACTTCACCAC CTATCCCAAA

451 ACCTGTAAGA ACTAATGATA ATCCATCACC CTTTGCTGAC TCTCTTTTCG

501 GACTCAGCCC GCCTGCACCC AGGTGAAATA AACAGCCATG TTGCTCACAC

551 AAAGCCTGTT TGGTGGTGTC TTCACACAGA CGCGCATGAA ACACATCTCT

601 ACTAAAAATA CAATAATCAG CTGGGCGAGG TGGCTCACAG CTGTAATCTC

651 AGCACTTTGG GAGGCCGAGA CAGGCAGGTC ACTTGAGGCC ATGAGTTCGA

701 GACCAGCCTG GCCAACATCG TGAAAACCCC ATCTCTACCA AAAATACAAA

751 AACTAGCCAG ATGTGGTGGC GCACGCCTGT AATCCCAGCT ACTCGGGAGG

801 CTGAGGTACC GAATCGTCTG AACGTGGGAA GTGGAGCTTG TAGTGAGCCG

851 AGATCGCCCC ACTGCACTCC AGCCTGGGCA ACAGAGCTAG ACTGTCTCAA

901 AACAAACAAA AAATGGTGTC AAGACTCTCA GACGAGATTC TAATGGATTA

951 AGGCCTATAT GTAAATAGCA CCAAAGACTA TGGAACAGAG ATGGGAGAAG

1001 CAAGCAGGGA GGCAGGAATA GTTTAGCTGT GGCAGTTTTA GCTTAGTCCA

1051 CTTACATAAA TGGTTCTTTA GGGTAGCACG TGGAGCATCC TCATTTCCAA

1101 ACATTGGACT GAGAGTAGAG AGCTGTGCAA AATAACCACA AGTCCCCAAC

1151 TATGCCCTCT TAATTATCCC TATCATCTAA GACTGTTGTT CCCATCCATC

1201 ACTGAACTTC CCCGTCCTCT TCCTTCAACC CCTGTGTTAG TCAATGGTTG

FIGURE 1 CONT'D

1251 AAATTTTGAT TTGGTAAAAA ACCTCTGGCG AAAACCAGCA AAAAGGGCTC

1301 ACAAATCAGG TCTCAGGGAA GCACAGAGGT AGCCACGAGA AGGCCCGAGG

1351 TGCTCATGGA AAGAGCTCGA GCCCAGGAGC TCTGGGAGGA CCCCAGGCGC

1401 TCGGAGCCGC CGTTACGTAA CCGGCACTCA GAGCCTCCGA AGACCGGAAG

1451 GCCCCGCTCA GGCCCCGGCC CCGGCCCCGG CCCCGCCCCG GCCCGGCCGG

1501 GCAGCTGGTA GGTGCCGTGC GCAACCCTCC GGAAGCTGCC GCCCCTTTCC

1551 CCTTTTATGG GAATACTTTT TTTAAAAAAA AAGAGTTCGC TGGCGCCACC

1601 CCGTAGGACT GGCCGCCCTA AAACCGTGAT AAAGGAGCTG CTCGCCACTT

1651 CTCACTTCCG CTTCCTTCCA GTAAGGAGTC GGGGTCTTCC CCAGTTTTCT

1701 CAGCCAGGCG GCGGCGGCGA CTGGCAatgT TTGGCCTCAA AAGAAACGCG

1751 GTAATCGGAC TCAACCTCTA CTGTGGGGGG GCCGGCTTGG GGGCCGGCAG

1801 CGGCGGCGCC ACCCGCCCGG GAGGGCGACT TTTGGCTACG GAGAAGGAGG

1851 CCTCGGCCCG GCGAGAGATA GGGGGAGGGG AGGCCGGCGC GGTGATTGGC

1901 GGAAGCGCCG GCGCAAGCCC CCCGTCCACC CTCACGCCAG ACTCCCGGAG

1951 GGTCGCGCGG CCGCCGCCCA TTGGCGCCGA GGTCCCCGAC GTCACCGCGA

2001 CCCCCGCGAG GCTGCTTTTC TTCGCGCCCA CCCGCCGCGC GGCGCCGCTT

2051 GAGGAGATGG AAGCCCCGGC CGCTGACGCC ATCATGTCGC CCGAAGAGGA

2101 GCTGGACGGG TACGAGCCGG AGCCTCTCGG GAAGCGGCCG GCTGTCCTGC

2151 CGCTGCTGGA GTTGGTCGGG GAATCTGGTA ATAACACCAG TACGGACGGG

2201 TCACTACCCT CGACGCCGCC GCCAGCAGAG GAGGAGGAGG ACGACTTGTA

2251 CCGGCAGTCG CTGGAGATTA TCTCTCGGTA CCTTCGGGAG CAGGCCACCG

2301 GCGCCAAGGA CACAAAGCCA ATGGGCAGGT CTGGGGCCAC CAGCAGGAAG

2351 GCGCTGGAGA CCTTACGACG GGTTGGGGAT GGCGTGCAGC GCAACCACGA

2401 GACGGCCTTC CAAGgtaagg gggttcatta atcgccaagg cctcactccc

2451 ttttttccat ctctccccgg actcactcgc caagggtggg ttggaaaccg

2501 aaacgagtca gtgttgaaac gtgtctcatc ctattcctga agccagaata

2551 ttctggccat gagtcattgt ttccgcccat cttgattctt ttggaaatgg

FIGURE 1 CONT'D

2601 cagctcttgt tcaaagaccg gaaagggtgg gatgtcaatt tcaagtgggg

2651 tcaacctgag ttctgtaaat cccagtagcg attttcccgc cgcgggtggg

2701 caggcgaatc ttgcgccggt ttagacaaag gaggccgtga ggacctgcat

2751 gcttttcttt ctcagGCATG CTTCGGAAAC TGGACATCAA AAACGAAGAC

2801 GATGTGAAAT CGTTGTCTCG AGTGATGATC CATGTTTTCA GCGACGGCGT

2851 AACAAACTGG GGCAGGATTG TGACTCTCAT TTCTTTTGGT GCCTTTGTGG

2901 CTAAACACTT GAAGACCATA AACCAAGAAA GCTGCATCGA ACCATTAGCA

2951 GAAAGTATCA CAGACGTTCT CGTAAGGACA AAACGGGACT GGCTAGTTAA

3001 ACAAAGAGGC TGGgtaagtt tgccttaagg atgaaagggg ccttggagtg

3051 gagtggaagt agaatgaagg attttttta gagaggtggg gatatctaaa

3101 ggtttttatg acgcacggct gtttgcaggc tctaactaaa ggaccattgt

3151 ttatttgatt tttaagtagt ggatccttag agatagtggt atggcggtct

3201 tgaattgtat caaaaatctt ggttttctct aggcaatttt ttgttccaat

3251 tcagttgaat actcttcagt ggattcaaac catgaaaaaa taagtcacca

3301 ggggaggata gctgaaataa ttcctaaggc ggtgcctgtt ttaatggaga

3351 agatatgggg tggagcctgc gttttaaaca aacccagatc tgatgcagga

3401 tgtacttaac tacgttgaga aaaactgatc tgcgcaattg aggcgttact

3451 gaaatattag gtggtggaga tttgagaata agggttttcg tcttttacct

3501 catgggaact ctggaagtcc ttttgttagg ataaatccta ataagacctt

3551 gatagtactg taaaatgaag tttaattatc atgggtcccc gcttaagaaa

3601 ctgaagaact tattttcttt ttttgccccg gggtgaataa taattggttt

3651 actattgctt taggggggaaa ccttagatat tttaatttac cttctctctg

3701 gatagtagtg ttgttaagag agcagaaacc cattcttgaa aatgtgcttt

3751 tctttttgt tttctagGAT GGGTTTGTGG AGTTCTTCCA TGTAGAGGAC

3801 CTAGAAGGTG GCATCAGGAA TGTGCTGCTG GCTTTTGCAG GTGTTGCTGG

3851 AGTAGGAGCT GGTTTGGCAT ATCTAATAAG AtagCCTTAC TGTAAGTGCA

3901 ATAGTTGACT TTTAACCAAC CACCACCACC ACCAAAACCA GTTTATGCAG

FIGURE 1 CONT'D

3951 TTGGACTCCA AGCTGTAACT TCCTAGAGTT GCACCCTAGC AACCTAGCCA

4001 GAAAAGCAAG TGGCAAGAGG ATTATGGCTA ACAAGAATAA ATACATGGGA

4051 AGAGTGCTCC CCATTGATTG AAGAGTCACT GTCTGAAAGA AGCAAAGTTC

4101 AGTTTCAGCA ACAAACAAAC TTTGTTTGGG AAGCTATGGA GGAGGACTTT

4151 TAGATTTAGT GAAGATGGTA GGGTGGAAAG ACTTAATTTC CTTGTTGAGA

4201 ACAGGAAAGT GGCCAGTAGC CAGGCAAGTC ATAGAATTGA TTACCCGCCG

4251 AATTCATTAA TTTACTGTAG TAGTGTTAAG AGAAGCACTA AGAATGCCAG

4301 TGACCTGTGT AAAAGTTACA AGTAATAGAA CTATGACTGT AAGCCTCAGT

4351 ACTGTACAAG GGAAGCTTTT CCTCTCTCTA ATTAGCTTTC CCAGTATACT

4401 TCTTAGAAAG TCCAAGTGTT CAGGACTTTT ATACCTGTTA TACTTTGGCT

4451 TGGTTCCATG ATTCTTACTT TATTAGCCTA GTTTATCACC AATAACACTT

4501 GACGGAAGGC TCAGTAATTA GTTATGAATA TGGATATCCT CAATTCTTAA

4551 GACAGCTTGT AAATGTATTT GTAAAAATTG TATATATTTT TACAGAAAGT

4601 CTATTTCCTT GAAACGAAGG AAGTATCGAA TTTACATTAG TTTTTTTCAT

4651 ACCCTTTTGA ACTTTGCAAC TTCCGTAATT AGGAACCTGT TTCTTACAGC

4701 TTTTCTATGC TAAACTTTGT TCTGTTCAGT TCTAGAGTGT ATACAGAACG

4751 AATTGATGTG TAACTGTATG CAGACTGGTT GTAGTGGAAC AAATCTGATA

4801 ACTATGCAGG TTTAAATTTT CTTATCTGAT TTTGGTAAGT ATTCCTTAGA

4851 TAGGTTTTCT TTGAAAACCT GGGATTGAGA GGTTGATGAA TGGAAATTCT

4901 TTCACTTCAT TATATGCAAG TTTTCAATAA TTAGGTCTAA GTGGAGTTTT

4951 AAGGTTACTG ATGACTTACA AATAATGGGC TCTGATTGGG CAATACTCAT

5001 TTGAGTTCCT TCCATTTGAC CTAATTTAAC TGGTGAAATT TAAAGTGAAT

5051 TCATGGGCTC ATCTTTAAAG CTTTTACTAA AAGATTTTCA GCTGAATGGA

5101 ACTCATTAGC TGTGTGCATA TAAAAAGATC ACATCAGGTG GATGGAGAGA

5151 CATTTGATCC CTTGTTTGCT TAATAAATTA TAAAATGATG GCTTGGAAAA

5201 GCAGGCTAGT CTAACCATGG TGCTATTATT AGGCTTGCTT GTTACACACA

5251 CAGGTCTAAG CCTAGTATGT CAATAAAGCA AATACTTACT GTTTTGTTTC

FIGURE 1 CONT'D

5301 TATTAATGAT TCCCAAACCT TGTTGCAAGT TTTTGCATTG GCATCTTTGG

5351 ATTTCAGTCT TGATGTTTGT TCTATCAGAC TTAACCTTTT ATTTCCTGTC

5401 CTTCCTTGAA ATTGCTGATT GTTCTGCTCC CTCTACAGAT ATTTATATCA

5451 ATTCCTACAG CTTTCCCCTG CCATCCCTGA ACTCTTTCTA GCCCTTTTAG

5501 ATTTTGGCAC TGTGAAACCC CTGCTGGAAA CCTGAGTGAC CCTCCCTCCC

5551 CACCAAGAGT CCACAGACCT TTCATCTTTC ACGAACTTGA TCCTGTTAGC

5601 AGGTGGTAAT ACCATGGGTG CTGTGACACT AACAGTCATT GAGAGGTGGG

5651 AGGAAGTCCC TTTTCCTTGG ACTGGTATCT TTTCAACTAT TGTTTTATCC

5701 TGTCTTTGGG GGCAATGTGT CAAAAGTCCC CTCAGGAATT TTCAGAGGAA

5751 AGAACATTTT ATGAGGCTTT CTCTAAAGTT TCCTTTGTAT AGGAGTATGC

5801 TCACTTAAAT TTACAGAAAG AGGTGAGCTG TGTTAAACCT CAGAGTTTAA

5851 AAGCTACTGA TAAACTGAAG AAAGTGTCTA TATTGGAACT AGGGTCATTT

5901 GAAAGCTTCA GTCTCGGAAC ATGACCTTTA GTCTGTGGAC TCCATTTAAA

5951 AATAGGTATG AATAAGATGA CTAAGAATGT AATGGGGAAG AACTGCCCTG

6001 CCTGCCCATC TCAGAGCCAT AAGGTCATCT TTGCTAGAGC TATTTTTACC

6051 TATGTATTTA TCGTTCTTGA TCATAAGCCG CTTATTTATA TCATGTATCT

6101 CTAAGGACCT AAAAGCACTT TATGTAGTTT TTAATTAATC TTAAGATCTG

6151 GTTACGGTAA CTAAAAGCCT GTCTGCCAAA TCCAGTGGAA ACAAGTGCAT

6201 AGATGTGAAT TGGTTTTTAG GGGCCCCACT TCCCAATTCA TTAGGTATGA

6251 CTGTGGAAAT ACAGACAAGG ACTTAGTTGA TATTTTGGGC TTGGGGCAGT

6301 GAGGGCTTAG GACACCCCAA GTGGTTTGGG AAAGGAGGAG GGAGTGGTGG

6351 GTTTATAGGG GAGGAGGAGG CAGGTGGTCT AAGTGCTGAC TGGCTACGTA

6401 GTTCGGGCAA ATCCTCCAAA AGGGAAAGGG AGGATTTGCT TAGAAGGATG

6451 GGGCTCCCAG TGACTACTTT TTGACTTCTG TTTGTCTTAC GCTTCTCTCA

6501 GGGAAAAACA TGCAGTCCTC TAGTGTTTCA TGTACATTCT GTGGGGGGTG

6551 AACACCTTGG TTCTGGTTAA ACAGCTGTAC TTTTGATAGC TGTGCCAGGA

6601 AGGGTTAGGA CCAACTACAA ATTAATGTTG GTTGTCAAAT GTAGTGTGTT

FIGURE 1 CONT'D

6651 TCCCTAACTT TCTGTTTTTC CTGAGAAAAA AAAATAAATC TTTTATTCAA

6701 ATAcagggtg tgatatgggt cttttctcat cgacgcctct ttttccttcc

6751 ctctcttagg caaacctttt agagaagtca gctgagcaaa tatgtacagg

6801 tggaattcaa agcaaaagcc tcacaaagtt gatttgcctt agagcaaagg

6851 acagttcctt cttcaattct aattagaggt gttgggtttt taattaaata

6901 tattactgct gtacttagag gagttcttaa acctccaagt aaaatcaaaa

6951 acctctttaa aatcaaaatt tctgtcttga tttatttatt tattattttt

7001 tttttgagat ggagttttgc tcttgttgtc caggctggag tgcaatggcc

7051 agatctccgc tcaccgcaac ctccgcctcc aggttcaaat gattctcctg

7101 cctcagcctc ctgagtagct gggaatacag gcatgcgcca ccacacccag

7151 ataattttgt atttttggta gagatggggt ttctccgtgt tggtcaggct

7201 ggtcttgaac tcccgacctc aggtgattgc ccacctctgc ctcccagagt

7251 gccaggatac aggcgtgagc catcgcaccc agcctctgtc ttgatttttt

7301 tgaatcacca ggtgttggta tgttttgttt tgttttgttt tgaggcacag

7351 tctcactctt ttgcccaggc tagagtgcag tggggcaatc tcggctcact

7401 gcaacctcag cctcccgagt agctgggatt acaggtgccc gccaccatgc

7451 ccggctaatt tttctatttt tggtagagac ggggttttgc cgtgttggtc

7501 aggctggttt gaagtcctga cctcagtgat ccactcgcct cagccgaagt

7551 gctgcgatta cagacctgag ccactgcgcc cagccttgat tttgaggtaa

7601 gagggtactt acagcagtta tctatcataa cacctaaata atacctaaag

7651 ttaaagagtt ttgatgaagt tcttggcagc agtgcttttc cccttctgct

7701 ttccaaaagg aggtaaaaag aagccagtca atttcaaaaa ccctatcctg

7751 cttttatttt cagctacctt gaaagtgagc tgaatcacca tggaaatgtg

7801 caaatgtgag gtttgcatac ttggttttaa gccctgagca ccatatgcta

7851 atcaggcaat caggattctg tgcctccctg cagtcagttg catttctatt

7901 taaaagtgca ttttggtttg gaagccccct ttggagccta actaccaaaa

7951 ggcagcaact ttttgtatca ttacaaagaa agctgtgtaa gtgcactccc

FIGURE 1 CONT'D

8001 aagcaaaggt gtggtaggag agtagcagcc acagaggacc caagcccaag

8051 tcttggcctg agttaagtta gtgctattgc tcccattgac gtgctatgat

8101 gtgaagccgt ttctggtaca gtgttccttt gctcagcacc ttaaaagctt

8151 ggatttaata gtaactgggt aaccttaatc agtagtcaga attatcaaca

8201 ctttgcttta tttgacacaa ccagactttc tcagttcctg ttctgtatct

8251 aga

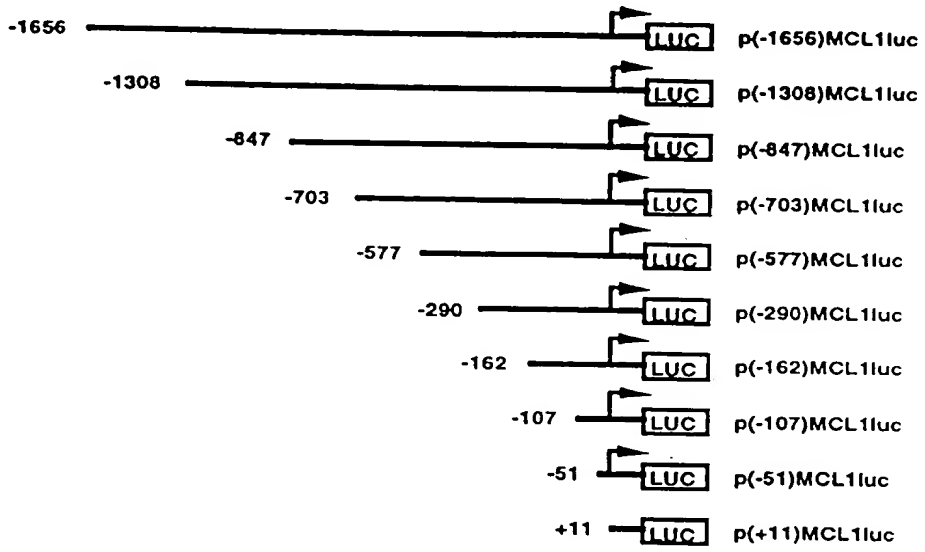

FIG. 2A

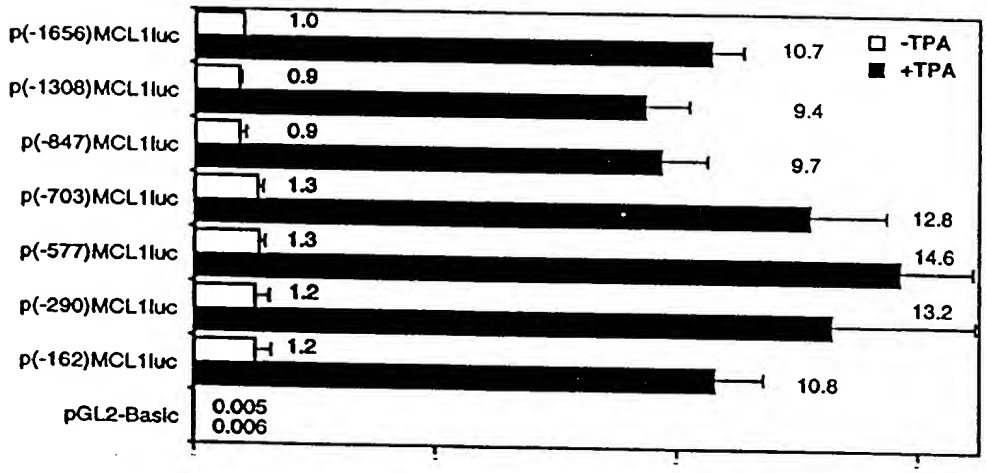

FIG. 2B

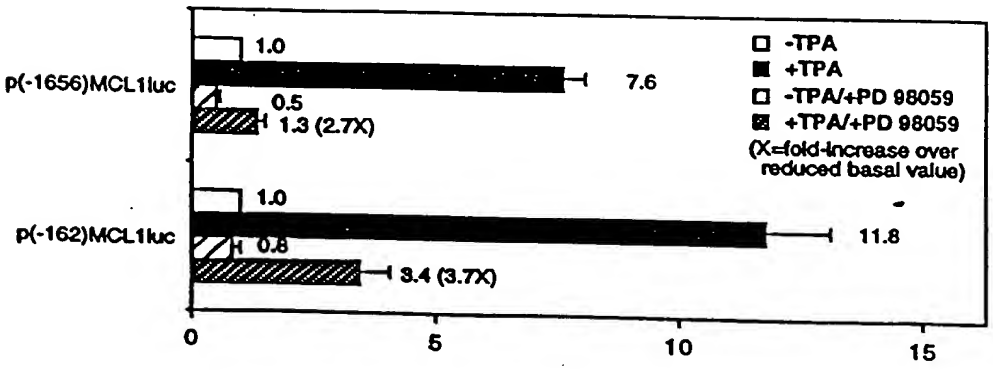

FIG. 2C

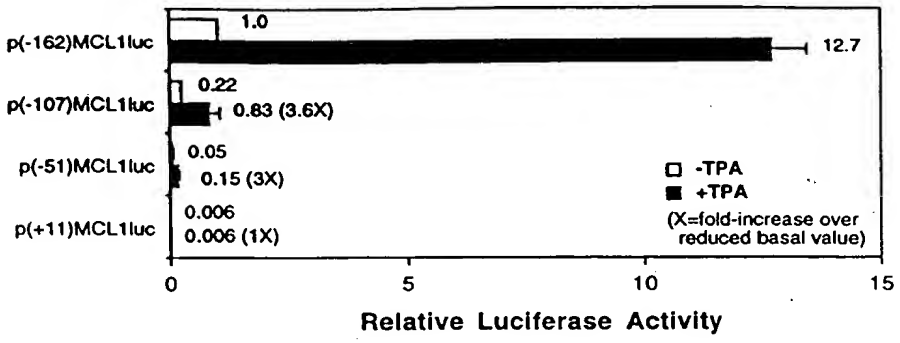

FIG. 3A

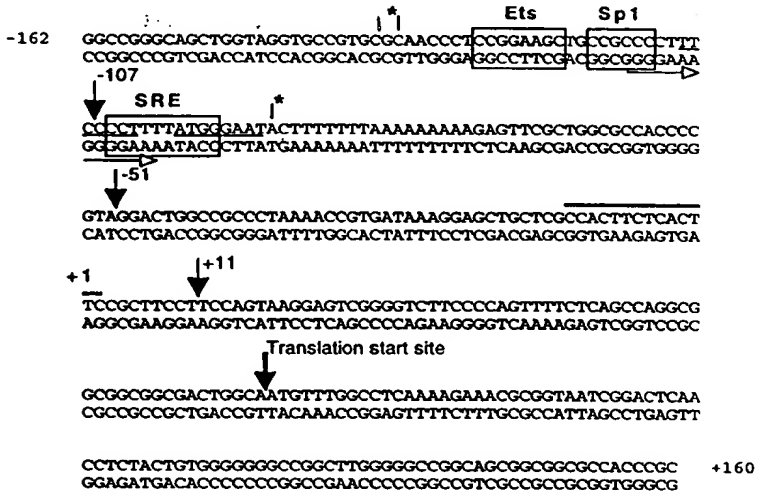

FIG. 3B

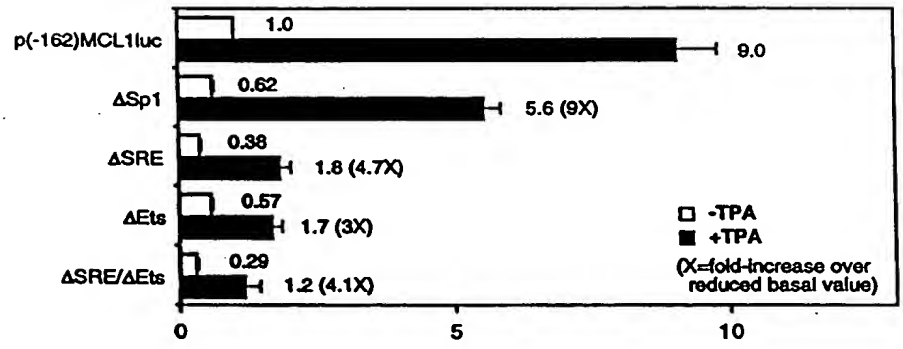

FIG. 3C

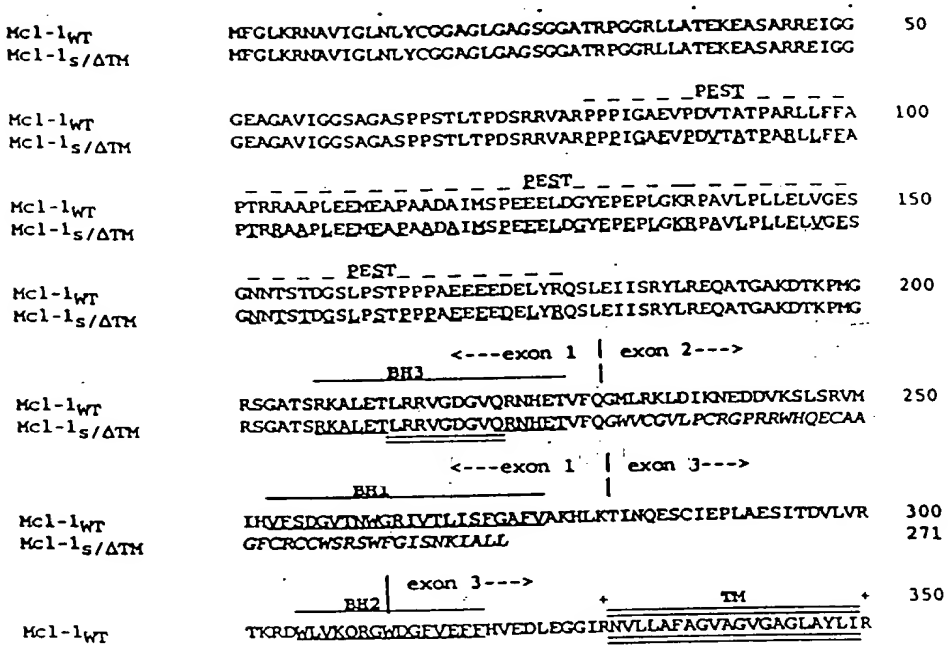
Mcl-1WT
Mcl-1s/ΔTM
MFGLKRNAVIGLNLYCGGAGLGAGSGGATRPGGRLLATEKEASARREIGG 50
PEST
GEAGAVIGGSAGASPPSTLTPDSRRVARPPPIGAEVPDVTATPARLLFFA 100
PTRRAAPLEEMEAPAADAIMSPEEELDGYEPEPLGKRPAVLPLLELVGES 150
PEST
GNNTSTDGSLPSTPPPAEEEEDELYRQSLEIISRYLREQATGAKDTKPMG 200
<---exon 1 | exon 2--->
BH3
RSGATSRKALETLRRVGDGVQRNHETVFQGMLRKLDIKNEDDVKSLSRVM 250
<---exon 1 | exon 3--->
BH1
IHVFSDGVTNWGRIVTLISFGAFVAKHLKTINQESCIEPLAESITDVLVR 300
GFCRCCWSRSWFGISNKIALL 271
exon 3---> TM 350
BH2
TKRDWLVKQRGWDGFVEFFHVEDLEGGIRNVLLAFAGVAGVGAGLAYLIR

FIG. 4A

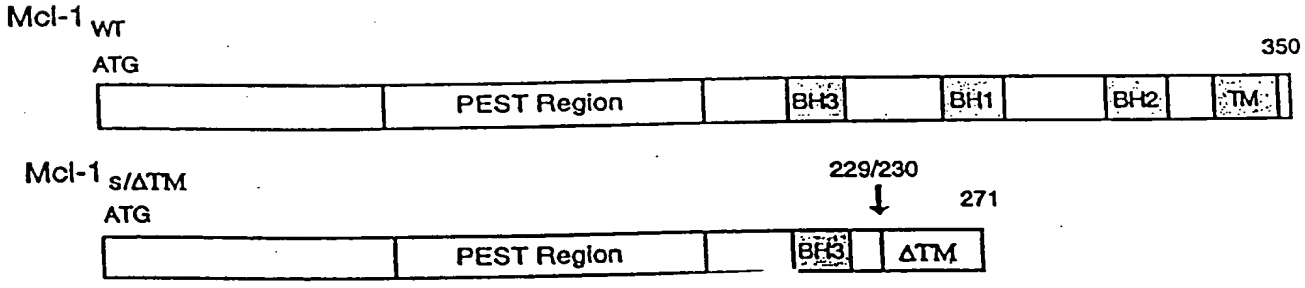
Mcl-1 WT
ATG
350
PEST Region
BH3
BH1
BH2
TM
Mcl-1 s/ΔTM
229/230
271
ATG
PEST Region
BH3
ΔTM

FIG. 4B

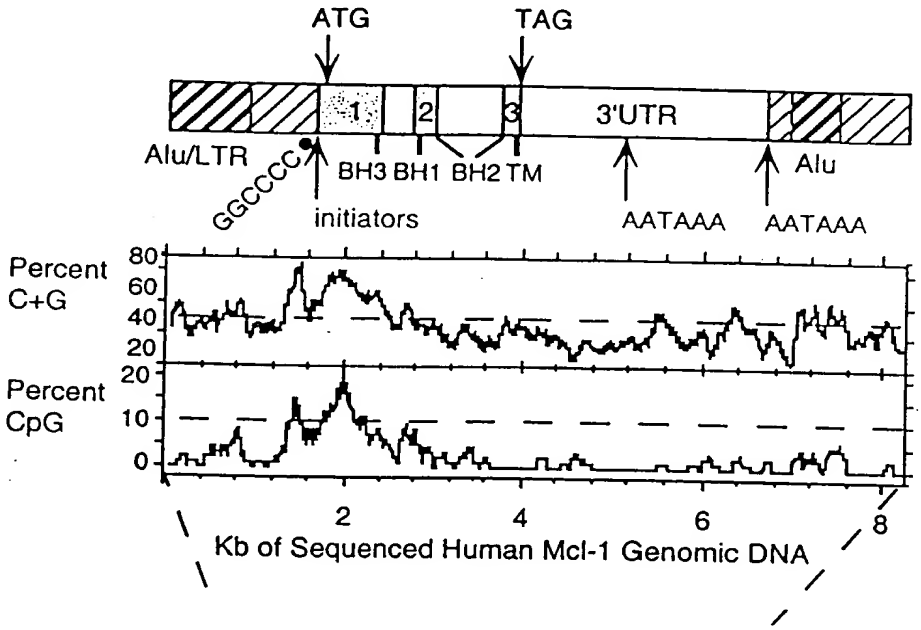
ATG
TAG
1
2
3
3'UTR
Alu/LTR
GGCCCC
BH3 BH1 BH2 TM
Alu
initiators
AATAAA
AATAAA
Percent C+G
80
60
40
20
Percent CpG
20
10
0
2
4
6
8
Kb of Sequenced Human Mcl-1 Genomic DNA

FIG. 5A

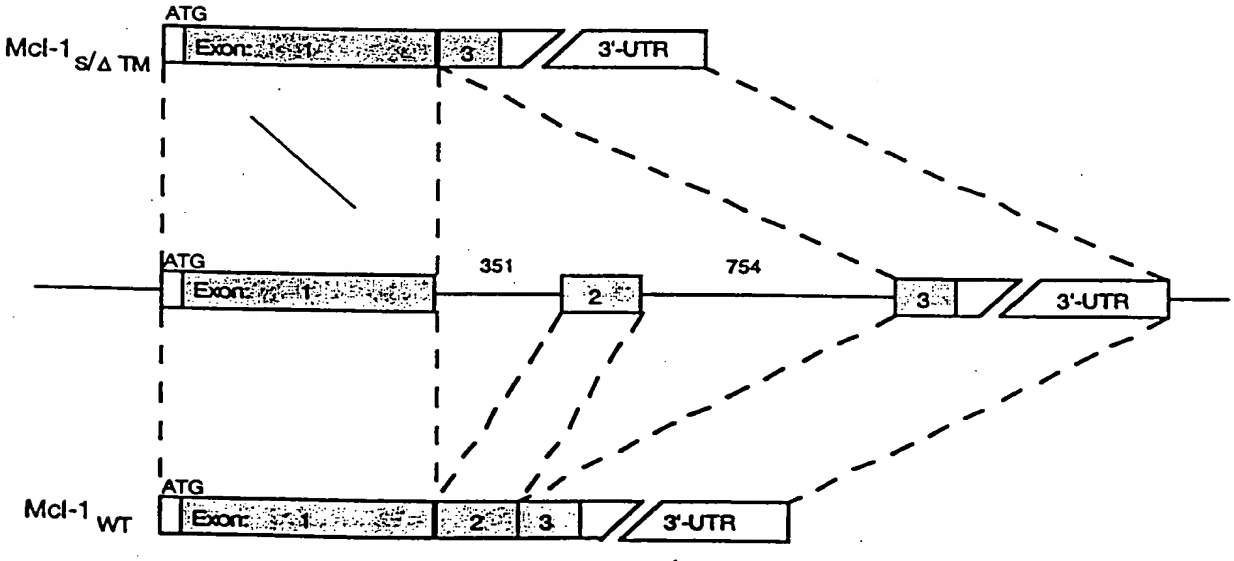
Mcl-1 s/Δ TM
ATG
Exon 1
3
3'-UTR
ATG
Exon 1
351
2
754
3
3'-UTR
Mcl-1 WT
ATG
Exon 1
2
3
3'-UTR

FIG. 5B